

## RAW SEQUENCE LISTING

DATE: 05/01/2002

PATENT APPLICATION: US/09/522,753B

TIME: 13:00:12

Input Set : A:\Salk1510.app

Output Set: N:\CRF3\05012002\I522753B.raw

287 Gly Gly Gly Lys Ala Lys Val Ser Gly Arg Pro Ser Ser Arg Lys Ala  
 288 1380 1385 1390  
 290 Lys Ser Pro Ala Pro Gly Leu Ala Ser Gly Asp Arg Pro Pro Ser Val  
 291 1395 1400 1405  
 293 Ser Ser Val His Ser Glu Gly Asp Cys Asn Arg Arg Thr Pro Leu Thr  
 294 1410 1415 1420  
 296 Asn Arg Val Trp Glu Asp Arg Pro Ser Ser Ala Gly Ser Thr Pro Phe  
 297 1425 1430 1435 1440  
 299 Pro Tyr Asn Pro Leu Ile Met Arg Leu Gln Ala Gly Val Met Ala Ser  
 300 1445 1450 1455  
 302 Pro Pro Pro Pro Gly Leu Pro Ala Gly Ser Gly Pro Leu Ala Gly Pro  
 303 1460 1465 1470  
 305 His His Ala Trp Asp Glu Glu Pro Lys Pro Leu Leu Cys Ser Gln Tyr  
 306 1475 1480 1485  
 308 Glu Thr Leu Ser Asp Ser Glu  
 309 1490 1495

312 &lt;210&gt; SEQ ID NO: 2

313 &lt;211&gt; LENGTH: 46

314 &lt;212&gt; TYPE: PRT

315 &lt;213&gt; ORGANISM: Homo sapiens

317 &lt;400&gt; SEQUENCE: 2

318 His Ser Asp Val Ser Glu Ser Lys Arg Lys Arg Phe Glu Leu Asn Ser  
 319 1 5 10 15  
 321 Gly Glu Ala Gly Gly Asn Ala Thr Ser Ala Met Thr Asn Ser Ser Thr  
 322 20 25 30  
 324 Ser Gly Ser Met Asn Ile Ser Asn Ser His Gly Leu Lys Ala  
 325 35 40 45

328 &lt;210&gt; SEQ ID NO: 3

329 &lt;211&gt; LENGTH: 17

330 &lt;212&gt; TYPE: DNA

331 &lt;213&gt; ORGANISM: Saccharomyces sp.

333 &lt;400&gt; SEQUENCE: 3

334 cggaggactg tcctccg

17

337 &lt;210&gt; SEQ ID NO: 4

338 &lt;211&gt; LENGTH: 8561

339 &lt;212&gt; TYPE: DNA

340 &lt;213&gt; ORGANISM: Homo sapiens

342 &lt;400&gt; SEQUENCE: 4

343 catgtcgggc tccacacagc ttgtggcaca gacgtggagg gccactgagc cccgctaccc 60  
 344 gccccacagc ctttcttacc cagtgcagat cgcccgagc cacacggacg tcgggctcct 120  
 345 ggagtaccag caccactccc gcgactatgc ctcccacctg tcgccgggct ccatcatcca 180  
 346 gccccagcgg cggaggccct ccctgctgtc tgagttccag cccgggaatg aacggtccca 240  
 347 ggagctccac ctgcggccag agtcccactc atacctgcc gagctgggga agtcagagat 300  
 348 ggagttcatt gaaagcaagc gccctcggct agagctgctg cctgaccccc tgctgcgacc 360  
 349 gtcacccctg ctggccacgg gccagcctgc gggatctgaa gacctacca aggaccgtag 420  
 350 cctgacgggc aagctggaac cgggtgtctc ccccagcccc ccgcacactg accctgagct 480  
 351 ggagctggtg ccgccacggc tgtccaagga ggagctgac cagaacatgg accgcgtgga 540  
 352 ccgagagatc accatggtag agcagcagat ctctaagctg aagaagaagc agcaacagct 600  
 353 ggaggaggag gctgccaagc cgcccagagc tgagaagccc gtgtcaccgc cgcccatcga 660